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NEWS 4 JUN 13 USPATFULL and USPAT2 updated with 11-character
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NEWS 6 JUN 25 CA/CAplus and USPAT databases updated with IPC
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NEWS 10 JUN 30 STN AnaVist enhanced with database content from EPFULL
NEWS 11 JUL 28 CA/CAplus patent coverage enhanced
NEWS 12 JUL 28 EPFULL enhanced with additional legal status
                 information from the epoline Register
NEWS 13 JUL 28 IFICDB, IFIPAT, and IFIUDB reloaded with enhancements
NEWS 14 JUL 28 STN Viewer performance improved
NEWS 15 AUG 01 INPADOCDB and INPAFAMDB coverage enhanced
NEWS 16 AUG 13 CA/CAplus enhanced with printed Chemical Abstracts
                 page images from 1967-1998
NEWS 17 AUG 15 CAOLD to be discontinued on December 31, 2008
NEWS 18 AUG 15 CAplus currency for Korean patents enhanced
NEWS 19 AUG 27 CAS definition of basic patents expanded to ensure
                 comprehensive access to substance and sequence
                 information
NEWS 20 SEP 18 Support for STN Express, Versions 6.01 and earlier,
                 to be discontinued
NEWS 21 SEP 25 CA/CAplus current-awareness alert options enhanced
                 to accommodate supplemental CAS indexing of
                 exemplified prophetic substances
NEWS 22 SEP 26 WPIDS, WPINDEX, and WPIX coverage of Chinese and
                 and Korean patents enhanced
NEWS 23 SEP 29 IFICLS enhanced with new super search field
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                 display fields

NEWS 25 SEP 30 CAS patent coverage enhanced to include exemplified
                 prophetic substances identified in new Japanese-
                 language patents
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NEWS 27 OCT 07 Multiple databases enhanced for more flexible patent
                 number searching
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                 enhanced
NEWS 29 OCT 22 WPIDS, WPINDEX, and WPIX enhanced with Canadian PCT
                 Applications

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DICTIONARY FILE UPDATES: 21 OCT 2008 HIGHEST RN 1064205-90-8

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L1   8 SWEFRT/SQSP

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FILE COVERS 1907 - 22 Oct 2008 VOL 149 ISS 17
FILE LAST UPDATED: 21 Oct 2008 (20081021/ED)

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=> l1
L2   10 L1

=> l2 and (pd<20040113)
     24770014 PD<20040113
             (PD<20040113)
L3   4 L2 AND (PD<20040113)

=> d l3 ibib abs hitstr 1-4

L3   ANSWER 1 OF 4 HCAPLUS COPYRIGHT 2008 ACS on STN
ACCESSION NUMBER: 2003:130956 HCAPLUS
DOCUMENT NUMBER: 138:199733
TITLE: A Drosophila full-length cDNA resource
AUTHOR(S):   Stapleton, Mark; Carlson, Joe; Brokstein, Peter; Yu,
                         Charles; Champe, Mark; George, Reed; Guarin, Hannibal;

```
                          Kronmiller, Brent; Pacleb, Joanne; Park, Soo; Wan,
                          Ken; Rubin, Gerald M.; Celniker, Susan E.
CORPORATE SOURCE:         Berkeley Drosophila Genome Project, Lawrence Berkeley
                          National Lab., Berkeley, CA, USA
SOURCE:                   GenomeBiology (2002), 3(12), No pp. given
                          CODEN: GNBLFW; ISSN: 1465-6914
                          URL: http://genomebiology.com/content/pdf/gb-2002-3-12-
                          research0080.pdf
PUBLISHER:                BioMed Central Ltd.
DOCUMENT TYPE:            Journal; (online computer file)
LANGUAGE:                 English
```

AB   A collection of sequenced full-length cDNAs is an important resource both
     for functional genomics studies and for the determination of the intron-exon
     structure of genes. Providing this resource to the Drosophila
     melanogaster research community has been a long-term goal of the Berkeley
     Drosophila Genome Project. The Drosophila Gene Collection (DGC) has been
     previously described , a set of putative full-length cDNAs that was
     produced by generating and analyzing >250,000 expressed sequence tags
     (ESTs) derived from a variety of tissues and developmental stages.
     High-quality full-insert sequence were generated for 8921 clones in the
     DGC. The sequences of these clones were compared to the annotated Release
     3 genomic sequence, and >5300 cDNAs identified that contain a complete and
     accurate protein-coding sequence. This corresponds to at least one splice
     form for 40% of the predicted D. melanogaster genes. Potential new cases
     of RNA editing were also identified. Thus, comparison of cDNA sequences
     to a high-quality annotated genomic sequence is an effective approach to
     identifying and eliminating defective clones from a cDNA collection.
     Clones were eliminated either because they carry single nucleotide
     discrepancies, which most probably result from reverse transcriptase
     errors, or because they are truncated and contain only part of the
     protein-coding sequence. [This abstract record is one of five records for
     this document necessitated by the large number of index entries required to
     fully index the document and publication system constraints.].

```
IT   481877-77-4
     RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
     (Biological study)
        (amino acid sequence; full-length cDNA sequence resource for Drosophila
        melanogaster)
RN   481877-77-4  HCAPLUS
CN   RE68566p (Drosophila melanogaster strain y; cn bw sp gene CG13893) (9CI)
     (CA INDEX NAME)
```

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

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L3   ANSWER 2 OF 4  HCAPLUS  COPYRIGHT 2008 ACS on STN
ACCESSION NUMBER:         2002:678785  HCAPLUS
DOCUMENT NUMBER:          137:380859
TITLE:                    R391: a conjugative integrating mosaic comprised of
                          phage, plasmid, and transposon elements
AUTHOR(S):                Boltner, Dietmar; MacMahon, Claire; Pembroke, J. Tony;
                          Strike, Peter; Osborn, A. Mark
CORPORATE SOURCE:         Department of Biological Sciences, University of
                          Essex, Colchester, CO4 3SQ, UK
SOURCE:                   Journal of Bacteriology (2002), 184(18),
                          5158-5169
                          CODEN: JOBAAY; ISSN: 0021-9193
```

PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB   The conjugative, chromosomally integrating element R391 is the archetype
      of the IncJ class of mobile genetic elements. Originally found in a South
      African Providencia rettgeri strain, R391 carries antibiotic and mercury
      resistance traits, as well as genes involved in mutagenic DNA repair.
      While initially described as a plasmid, R391 has subsequently been shown
      to be integrated into the bacterial chromosome, employing a phage-like
      integration mechanism closely related to that of the SXT element from
      Vibrio cholerae O139. Anal. of the complete 89-kb nucleotide sequence of
      R391 has revealed a mosaic structure consisting of elements originating in
      bacteriophages and plasmids and of transposable elements. A total of 96
      open reading frames were identified; of these, 30 could not be assigned a
      function. Sequence similarity suggests a relationship of large sections
      of R391 to sequences from Salmonella, in particular those corresponding to
      the putative conjugative transfer proteins, which are related to the
      IncHI1 plasmid R27. A composite transposon carrying the kanamycin
      resistance gene and a novel insertion element were identified.
      Challenging the previous assumption that IncJ elements are plasmids, no
      plasmid replicon was identified on R391, suggesting that they cannot
      replicate autonomously.
IT   476016-57-6
      RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
      (Biological study)
         (amino acid sequence; R391, a conjugative integrating mosaic comprised
         of phage, plasmid, and transposon elements)
RN   476016-57-6 HCAPLUS
CN   Protein (Providencia rettgeri mobile element R391 255-amino acid) (9CI)
      (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 74   THERE ARE 74 CITED REFERENCES AVAILABLE FOR THIS
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L3   ANSWER 3 OF 4 HCAPLUS COPYRIGHT 2008 ACS on STN
ACCESSION NUMBER: 2002:173239 HCAPLUS
DOCUMENT NUMBER: 136:396932
TITLE: Reagents and kits, such as nucleic acid arrays, for
                          detecting the expression of over 10,000 Drosophila
                          genes
INVENTOR(S):   Venter, J. Craig; Adams, Mark; Li, Peter W. D.; Myers,
                          Eugene W.
PATENT ASSIGNEE(S):   PE Corporation (NY), USA
SOURCE: PCT Int. Appl., 21 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 10
PATENT INFORMATION:

      PATENT NO.   KIND   DATE   APPLICATION NO.   DATE
      --------------   ----   -------- --------------------   --------
      WO 2001071042   A2   20010927 WO 2001-XG9231   20010323 <--
         W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,

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                HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
                LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,
                RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,
                YU, ZA, ZW
            RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
                DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
                BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
        WO 2001071042        A2     20010927   WO 2001-US9231        20010323 <--
        WO 2001071042        A3     20030313
             W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
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                HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
                LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,
                RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,
                YU, ZA, ZW
            RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
                DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
                BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
        US 20050208558       A1     20050922   US 2005-97143         20050404
PRIORITY APPLN. INFO.:                         US 2000-191637P   P   20000323
                                               US 2000-614150    A   20000711
                                               WO 2001-US9231    A   20010323
                                               US 1999-157832P   P   19991019
                                               US 1999-160191P   P   19991019
                                               US 1999-161932P   P   19991019
                                               US 1999-164769P   P   19991112
                                               US 1999-173383P   P   19991228
                                               US 2000-175693P   P   20000112
                                               US 2000-184831P   P   20000224
```

AB   The present invention is based on the sequencing and assembly of the
      Drosophila melanogaster genome. The present invention provides the
      primary nucleotide sequence of a large portion of the Drosophila
      melanogaster genome in a series of genomic and predicted transcript
      sequences. This information is provided in the form of genomic,
      transcript and protein sequence information and can be used to generate
      nucleic acid detection reagents and kits such as nucleic acid arrays.
      Primary sequences are provided as contiguous strings in a
      computer-readable format and recorded on media such as floppy disks, hard
      disks, magnetic tape, CD-ROM, RAM, ROM and hybrids of these categories.
      Genes/exons can be predicted,sequences can be edited and homol. searches
      of target motifs can be conducted. [This abstract record is one of ten
      records for this document necessitated by the large number of index entries
      required to fully index the document and publication system constraints.].
```
IT    431288-23-2
      RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological
      use, unclassified); PRP (Properties); ANST (Analytical study); BIOL
      (Biological study); USES (Uses)
         (amino acid sequence; reagents and kits, such as nucleic acid arrays,
         for detecting the expression of over 10,000 Drosophila genes)
RN    431288-23-2  HCAPLUS
CN    Protein (Drosophila melanogaster clone WO0171042-SEQID-33039) (9CI)  (CA
      INDEX NAME)
```

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3   ANSWER 4 OF 4 HCAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:230405 HCAPLUS
DOCUMENT NUMBER: 132:304167
TITLE: The genome sequence of Drosophila melanogaster
AUTHOR(S):   Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.;
                        Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides,
                        Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins,
                        Roger A.; Galle, Richard F.; George, Reed A.; Lewis,
                        Suzanna E.; Richards, Stephen; Ashburner, Michael;
                        Henderson, Scott N.; Sutton, Granger G.; Wortman,
                        Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin
                        X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej,
                        Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan,
                        Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt,
                        Gregg; Nelson, Catherine R.; Miklos, George L. Gabor;
                        Abril, Josep F.; Agbayani, Anna; An, Hui-Jin;
                        Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew,
                        Richard M.; Basu, Anand; Baxendale, James;
                        Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen
                        Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari,
                        Deepali; Bolshakov, Slava; Borkova, Dana; Botchan,
                        Michael R.; Bouck, John; Brokstein, Peter; Brottier,
                        Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler,
                        Heather; Cadieu, Edouard; Center, Angela; Chandra,
                        Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke,
                        Carl; Davenport, Lionel B.; Davies, Peter; De Pablos,
                        Beatriz; Delcher, Arthur; Deng, Zuoming; Mays, Anne
                        Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson,
                        Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha,
                        Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin,
                        Kenneth J.; Evangelista, Carlos C.; Ferraz,
                        Concepcion; Ferriera, Steven; Fleischmann, Wolfgang;
                        Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.;
                        Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong,
                        Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan,
                        Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon;
                        Heiman, Thomas J.; Hernandez, Judith R.; Houck,
                        Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland,
                        Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali,
                        Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi;
                        Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce
                        E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz,
                        Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei,
                        Yiding; Levitsky, Alexander A.; Li, Jiayin; Li,
                        Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun;
                        Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael
                        P.; McPherson, Duncan; Merkulov, Gennady; Milshina,
                        Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi,
                        Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian;
                        Murphy, Lee; Muzny, Donna M.; Nelson, David L.;
                        Nelson, David R.; Nelson, Keith A.; Nixon, Katherine;
                        Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo,
                        Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John;
                        Puri, Vinita; Reese, Martin G.; Reinert, Knut;
                        Remington, Karin; Saunders, Robert D. C.; Scheeler,
                        Frederick; Shen, Hua; Shue, Bixiang Christopher;
                        Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian

P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.;
Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas,
Robert; Tector, Cyndee; Turner, Russell; Venter, Eli;
Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman,
David A.; Weinstock, George M.; Weissenbach, Jean;
Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.;
Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh,
Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang,
Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun
H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu,
Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs,
Richard A.; Myers, Eugene W.; Rubin, Gerald M.;
Venter, J. Craig

AB   The fly Drosophila melanogaster is one of the most intensively studied
     organisms in biol. and serves as a model system for the investigation of
     many developmental and cellular processes common to higher eukaryotes,
     including humans. The nucleotide sequence was determined of nearly all of the
     .apprx.120-megabase euchromatic portion of the Drosophila genome using a
     whole-genome shotgun sequencing strategy supported by extensive
     clone-based sequence and a high-quality bacterial artificial chromosome
     phys. map. Efforts are under way to close the remaining gaps; however,
     the sequence is of sufficient accuracy and contiguity to be declared
     substantially complete and to support an initial anal. of genome structure
     and preliminary gene annotation and interpretation. The genome encodes
     .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis
     elegans genome, but with comparable functional diversity. Access to
     supporting information on each gene is available through FlyBase at
     http://flybase.bio.indiana.edu and through Celera at www.celera.com; the
     sequences are deposited in GenBank with Accession Nos. AE002566-AE003403.
     [This abstract record is one of 4 records for this document necessitated by
     the large number of index entries required to fully index the document and
     publication system constraints.].
IT   262973-73-9
     RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
     (Biological study)
        (amino acid sequence; genome sequence of Drosophila melanogaster)
RN   262973-73-9 HCAPLUS
CN   Protein (Drosophila melanogaster gene CG13893) (9CI) (CA INDEX NAME)

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FULL ESTIMATED COST   21.15   52.22

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L4   1 481877-77-4/RN

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L4   ANSWER 1 OF 1 REGISTRY COPYRIGHT 2008 ACS on STN
RN   481877-77-4 REGISTRY
CN   RE68566p (Drosophila melanogaster strain y; cn bw sp gene CG13893) (9CI)
     (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AAL49263
CN   GenBank AAL49263 (Translated from: GenBank AY071641)
FS   PROTEIN SEQUENCE
SQL 407

SEQ   1 MSGPLPEISE EQRAILEKFR KQMDDALVGT HDDYFLVRWL RARKWNLEAA

10/540,551

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101 FANFDMWGMM HCVTRFEFQK YLVLLLERFM KIAYDQSQKH GWRARQLVVF
151 FDMQDVNLKQ YAWRPAAECV ISTVKQYEAN FPELLKMCYI INAPKLFSVA
201 FNIVKKFLDE NTTSKIVIYK SGVDRWQEQL FSHVNRKAFP KAWGGEMVDR
251 NGDPQCKALM VWGGKLPEEL YIDQSSQQSD RDFVEAQVPK GDKLKLHFKV
301 NVEEQKILSW EFRTFDYDIK FGIYSVDDKT GEKRSEVPLG TVYSNEMDEI
351 GYISTRPNTT YTVVFDNSAS YLRSKKLRYW VDLISEEEEG ISELTTQMDN
401 TQIANQQ
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              1 REFERENCES IN FILE CA (1907 TO DATE)
              1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

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FULL ESTIMATED COST   14.93   67.15

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STRUCTURE FILE UPDATES: 21 OCT 2008 HIGHEST RN 1064205-90-8
DICTIONARY FILE UPDATES: 21 OCT 2008 HIGHEST RN 1064205-90-8

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH July 5, 2008.

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

REGISTRY includes numerically searchable data for experimental and

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predicted properties as well as tags indicating availability of
experimental property data in the original document. For information
on property searching in REGISTRY, refer to:

http://www.cas.org/support/stngen/stndoc/properties.html

=> S 476016-57-6/RN

L5   1 476016-57-6/RN

=> SET NOTICE 1 DISPLAY

NOTICE SET TO 1 U.S. DOLLAR FOR DISPLAY COMMAND
SET COMMAND COMPLETED

=> D L5 SQIDE 1-

YOU HAVE REQUESTED DATA FROM 1 ANSWERS - CONTINUE? Y/(N):y
THE ESTIMATED COST FOR THIS REQUEST IS 6.65 U.S. DOLLARS
DO YOU WANT TO CONTINUE WITH THIS REQUEST? (Y)/N:y

L5   ANSWER 1 OF 1 REGISTRY COPYRIGHT 2008 ACS on STN
RN   476016-57-6 REGISTRY
CN   Protein (Providencia rettgeri mobile element R391 255-amino acid) (9CI)
     (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AAM08029
CN   GenBank AAM08029 (Translated from: GenBank AY090559)
FS   PROTEIN SEQUENCE
SQL 255

SEQ   1 MMEKCFALYR YSHSDGTAKE WAIYVGSDTQ EIEVRFGKAG QMSQQRLIDS
       51 TDPNAEADRR INEKINKGYR FVGQVGIDHQ GRPFELSNAL DSVACANNVS
      101 WEFRTRKDVN GQISLAQKAL FDMAKLLEAY GLAVIDDNQV RIGKWSLGFC
      151 KSGLPSTNQI SMVSGEGAGI VNTDDGPWPL LLLLAFKRQL PPLCSLTVAS
      201 PEGIEVSDQL KLEKDVLRLL GSDLERVRPI AEALDLMPAK IDLNQSSPDS
      251 QNYYF
MF   Unspecified
CI   MAN
SR   CA
LC   STN Files: CA, CAPLUS, TOXCENTER
DT.CA CAplus document type: Journal
RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)
           1 REFERENCES IN FILE CA (1907 TO DATE)
           1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> SET NOTICE LOGIN DISPLAY

NOTICE SET TO OFF FOR DISPLAY COMMAND
SET COMMAND COMPLETED

=>